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(54) Title: GENOTYPING VARIABLE NUMBER TANDEM REPEATS

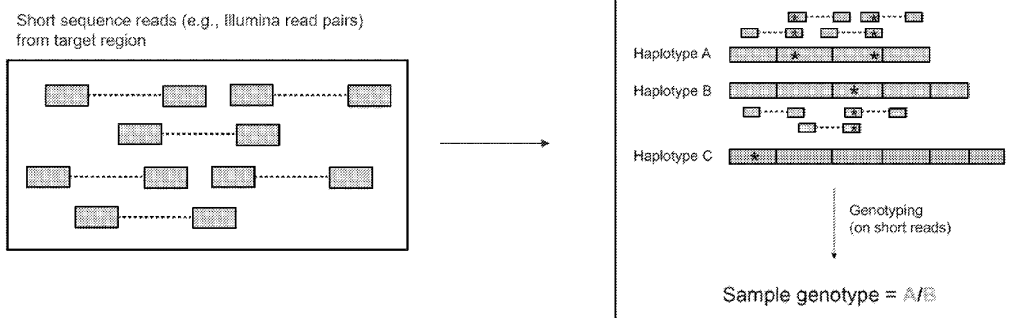


FIG. 4

(57) Abstract: Disclosed herein include systems, devices, and methods for determining a variable number tandem repeat (VNTR) status. Haplotypes of a VNTR can be determined using long sequence reads of reference samples aligned to the VNTR in a reference. Short reads of a test sample of a test subject can be aligned to the haplotypes determined using the long sequence reads to determine a VNTR status (e.g., one or more haplotypes or a genotype of the test subject) of the test subject based on the probability indications of the haplotypes.

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